IN THE SPECIFICATION

Please amend the Specification at page 11, line 13 through page 13, line 23 in the following manner:

~~Figure 1 shows nucleic acid sequences of AtFtn2 (ARC6 gene) from a wild type plant in a WS ecotype and of arc6-1 gene in an arc6-1 mutant plant in a WS-like ecotype. Panel A shows a cDNA sequence (SEQ ID NO:1), and panel B shows a genomic sequence (SEQ ID NO:3) of AtFtn2 gene; panel C shows a cDNA sequence (SEQ ID NO:9) and panel D shows a genomic sequence (SEQ ID NO:10) of arc6-1 gene.~~

~~Figure 2 shows the amino acid sequences of the peptide encoded by AtFtn2 (ARC6 gene) from a wild type plant in a WS ecotype (panel A, SEQ ID NO:2) and of the peptide encoded by arc6-1 gene in an arc6-1 mutant plant in a WS-like ecotype (panel B, SEQ ID NO:11).~~

~~Figure 3~~ Figure 1 shows the structure of the *AtFtn2* gene (Panel A) and protein (Panel B). Panel A shows that the open reading frame is terminated by a TAA in-frame stop codon. The diagram depicts introns (thin lines) and exons (black boxes). Sizes are given in bp. The position of the *arc6-1* mutation (C -> T) at position 1141 is marked. The nucleotide sequences flanking the mutation (underlined) show the change of codon 325 (CGA in a wild type plant) into a premature stop (TGA) in *arc6-1*. Panel B shows the putative functional and conserved protein domain, which are depicted as wider black boxes; their numerical positions within the AtFtn2 sequence are also indicated. Black lines above the diagram delineate regions of AtFtn2 conserved among Ftn2 homologues ~~(see Figures 4-6)~~. CT, chloroplast targeting signal.

Figure 2~~Figure 4~~ shows a sequence alignment of DnaJ-like domains of plant and cyanobacterial Ftn2 proteins (indicated by asterisk) and DnaJ domains from Pfam database. Total about 270 DnaJ domains from the database were aligned with the ARC6 proteins. Shown in this figure are only selected DnaJ domains most similar to Ftn2 proteins. Black and gray columns indicate that identical or similar amino acid, respectively, was present in 70% of all aligned sequences at that position. The TrEMBL accession codes and location of the DnaJ domain within the protein are shown for the Pfam database records. For the ARC6 homologues, if the protein sequences were derived

from EST records and did not encompass the initial M, the location of the DnaJ domain is not given.

Figure 3~~Figure 5~~ shows an alignment of plant and cyanobacterial Ftn2 full and partial sequences. Partial sequences are marked by asterisk (*). Not shown are the N-termini of the plant sequences, which contain chloroplast transit peptides. Light-gray and black columns indicate similarity and identity, respectively, greater than 80%. Gaps are indicated by a dash (-), missing sequence by an underline (_). Similarity and identity calculations do not include missing sequences. The Dna-J like domain is indicated by a solid line (▪▪▪)~~solid line (—)~~ Putative myb domain is indicated by diamonds (♦)~~diamonds (—)~~. Site of truncation of the protein in *arc6* mutant is marked by a triangle (▲)~~triangle (—)~~ at position 398 of the alignment (residue 325 of AtFtn2).

~~Figure 6 shows the nucleotide sequence (panel A , SEQ ID NO:4) and amino acid sequence (panel B , SEQ ID NO:5) of *ftn2* from *Synechococcus* sp. PCC 7942; these sequences have been submitted to GenBank under accession no. AF21196.~~

~~Figure 7 shows the nucleotide sequence (panel A , SEQ ID NO:6) and amino acid sequence (panel B, SEQ ID NO:7) of *ftn6* from *Synechococcus* sp. PCC 7942; these sequences have been submitted to GenBank under accession no. AF21197.~~

~~Figure 8 shows nucleotide and amino acid sequences of Ftn2 homologs described in Table 3.~~

~~Figure 9 shows the nucleic acid sequence of SEQ ID NO:11.~~

~~Figure 10 shows the nucleic acid sequence of SEQ ID NO:12.~~

~~Figure 11 shows the amino acid sequence of SEQ ID NO:13.~~

~~Figure 12 shows the nucleic acid sequence of SEQ ID NO:14.~~

~~Figure 13 shows the nucleic acid sequence of SEQ ID NO:15.~~

~~Figure 14 shows the amino acid sequence of SEQ ID NO:16.~~

~~Figure 15 shows the amino acid sequence of SEQ ID NO:17.~~

~~Figure 16 shows the amino acid sequence of SEQ ID NO:18.~~

~~Figure 17 shows the nucleic acid sequence of SEQ ID NO:19.~~

~~Figure 18 shows the nucleic acid sequence of SEQ ID NO:20.~~

~~Figure 19 shows the amino acid sequence of SEQ ID NO:21.~~

~~Figure 20 shows the nucleic acid sequence of SEQ ID NO:22.~~

~~Figure 21 shows the nucleic acid sequence of SEQ ID NO:23.~~

~~Figure 22 shows the amino acid sequence of SEQ ID NO:24.~~

~~Figure 23 shows the nucleic acid sequence of SEQ ID NO:25.~~

~~Figure 24 shows the genomic sequence of AtFzo-like gene. The sequences is the reverse complementary sequence; stop and start codons are indicated by underlined bold text~~

~~SEQ ID NO:26 is the genomic sequence; SEQ ID NO:27 comprises the sequence between and including the stop and start codons.~~

Figure 4~~Figure 25~~ shows an alignment of the AtARC5 gene with Dynamin-1 from *Homo sapiens* and Dnm1p from *Saccharomyces cerevisiae*. Gray boxes indicate completely conserved residues; yellow boxes are identical residues; cyan boxes are similar residues; dashes indicate gaps. The domain structure is indicated by the lines above the alignment. Red, GTPase domain; green, middle domain; blue, PH domain; lavender, GTPase effector domain; black, PR domain. The dotted underline indicates the sequence encoded by the alternatively spliced intron in *ARC5*. The triangle indicates the position of the *arc5* mutation.

~~Figure 26 shows additional sequences which are homologous to *AtARC5* gene.~~

~~Figure 27 shows additional sequences which are homologous to *AtFzo-like* gene.~~

Please amend the Specification at page 40, line 24 through page 41, line 3 in the following manner:

The product of the cyanobacterial *Ftn2* gene from *Synechococcus* sp. strain PCC 7942 was discovered to share a similarity with an unknown protein of *Arabidopsis thaliana* (AB016888|Q9FIG9; BLAST score, 72.8; Expect = 1×10^{-11}). It was therefore contemplated that this ortholog was involved in plastid division in Arabidopsis cells. The encoded product of this Arabidopsis *Ftn2* ortholog was predicted to posses a chloroplast transit peptide (from a web-based program (http://, followed by, HypothesisCreator.net/iPSORT/), with the amino acid sequence MEALS HVGIG LSPFQ LCRLP PATTK LRRSH. The Arabidopsis protein was also predicted to possess a DnaJ

domain profile according to ProfileScan (http://, followed by, www.isrec.isb-sib.ch/software/PFSCAN_form.html), and a Myb DNA-binding domain, according to InterProScan (http://www, followed by,.ebi.ac.uk/interpro/scan.html).

Please amend the Specification at page 41, lines 4-9 in the following manner:

The inventors subsequently identified, sequenced and characterized the orthologous gene and protein from Arabidopsis (SEQ ID NOs: 1, 2, 3, 9, 10 and 11~~see Figures 1 and 2~~). Based upon these results, the inventors discovered a novel chloroplast division gene in *Arabidopsis thaliana*; because chloroplast division gene in *Arabidopsis thaliana* is a homologue of the recently identified cell division gene *Ftn2* from a cyanobacterium *Synechococcus*, the Arabidopsis gene is designated *AtFtn2.*

Please amend the Specification at 42, line 28 through page 43, line 7 in the following manner:

The present invention provides compositions comprising an isolated nucleic acid sequence comprising prokaryotic-type division and related genes; in particular embodiments, the invention provides compositions comprising isolated *Ftn2, ARC5,* or *Fzo-like* genes. In some embodiments, the sequences comprise plant *Ftn2, ARC5,* or *Fzo-like* gene; in other embodiments, the sequences comprise Arabidopsis *Ftn2, ARC5,* or *Fzo-like* genes; in other embodiments, the sequences comprise algal *Ftn2, ARC5,* or *Fzo-like* genes; in other embodiments, the sequences comprise cyanobacterial *Ftn2, ARC5,* or *Fzo-like* genes. In different specific embodiments, isolated nucleic acid sequences comprise a nucleic acid sequence as ~~shown in the Figures and/or as~~ described in, for example, Table 3, or encode an amino acid sequence as ~~shown in the Figures and/or as~~ described in, for example, Table 3.

Please amend the Specification at page 43, lines 8-16 in the following manner:

The present invention also provides compositions comprising an isolated nucleic acid sequence comprising an antisense sequence of prokaryotic-type division and related genes; in particular embodiments, the antisense sequences are directed to *Ftn2, ARC5,* or

Fzo-like genes. In some embodiments, the sequences comprise an antisense sequence of a plant *Ftn2, ARC5,* or *Fzo-like* gene; in other embodiments, the sequences comprise an antisense sequence of an Arabidopsis *Ftn2, ARC5,* or *Fzo-like* gene; in other embodiments, the sequences comprise an antisense sequence of a cyanobacterial *Ftn2, ARC5,* or *Fzo-like* gene. In different specific embodiments, the sequences comprise antisense sequences of the sequences ~~shown in the Figures and~~ described, for example, in Table 3.

Please amend the Specification at page 43, line 23 through page 44, line 3 in the following manner:

The present invention provides compositions comprising purified prokaryotic-type division and related polypeptides; in particular embodiments, the polypeptides comprise Ftn2, ARC5, or Fzo-like polypeptides, as well as compositions comprising variants, homologs, mutants or fusion proteins thereof. In some embodiments, the polypeptide comprises a plant Ftn2, ARC5, or Fzo-like polypeptide; in other embodiments, the polypeptide comprises an Arabidopsis Ftn2, ARC5, or Fzo-like polypeptide; in other embodiments, the polypeptide comprises an algal Ftn2, ARC5, or Fzo-like polypeptide; in yet other embodiments, the polypeptide comprises a cyanobacterial Ftn2, ARC5, or Fzo-like polypeptides. In different specific embodiments, the polypeptide is encoded by a nucleic acid sequence ~~as shown in the Figures and/or~~ as described in, for example, Tables 3, 10, and 11, or comprises an amino acid sequence ~~as shown in the Figures and/or~~ as described in, for example, Tables 3, 10 and 11.

Please amend the Specification at page 45, line 11 through 22 in the following manner:

In some embodiments, ARC5 is also a fairly large protein of almost 800 amino acids; exemplary but non-limiting sequences are provided in SEQ ID NOs: 13 and 16-18~~Figures 11, 14, 15, and 16~~. In Arabidopsis, ARC5 exists in two forms, a longer form and a shorter form. The amino acid sequences of ARC5 were deduced from the cDNA sequence; the long form of the cDNA encodes a protein of 777 amino acids and 87.2 kDa, whereas the shorter form of the cDNA encodes a protein of 741 amino acids and

83.5 kDa. In addition, the ARC5 protein contains three motifs found in other dynamin-like proteins: a conserved N-terminal GTPase domain, a pleckstrin homology (PH) domain shown in some proteins to mediate membrane association, and a C-terminal GTPase Effector Domain (GED) thought to interact directly with the GTPase domain and to mediate self-assembly. The shorter cDNA encoded a protein of 741 amino acids and 83.5 kDa identical to that of the larger gene product except for the absence of 36 amino acids encoded by the sequence of the 15th intron.

Please amend the Specification at page 46, lines 6-12 in the following manner:

In some embodiments, an Fzo-like protein is also fairly large, of slightly more than about 640 amino acids; exemplary but non-limiting sequences are provided in SEQ ID NOs: 21 and 24~~Figures 19 and 22~~. In Arabidopsis, an Fzo-like of about 642 amino acids has a predicted chloroplast transit peptide, a GTPase domain and two a predicted trans-membrane domains. The evidence described in Example 7 indicates that Fzo-like proteins are involved in plastid division and/or morphology. In some embodiments, An Fzo-like polypeptide[[.]]

Please amend the Specification at page 60, lines 4-10 in the following manner:

The amino acid sequences of plant and cyanobacterial Ftn2 proteins were searched for protein motifs. One motif is a putative DnaJ domain (AtFtn2 residues 89-153; Scc_ PCC 7942_Ftn2 residues 6-70) as determined by the InterProScan program (InterPro accession IPR001623, Pfam conserved domain pfam00226). However, ClustalW alignment of this domain with all predicted DnaJ domains from the Pfam database (277 sequences) revealed that the central HPD motif essential for DnaJ proteins is not present in AtFtn2 or other plant and cyanobacterial ftn2 homologues (~~see Figure 4~~see Figure 2).

Please amend the Specification at page 60, lines 11-14 in the following manner:

Another domain discovered through a Pfam-HMM search in the plant Ftn2 proteins is a putative myb domain (residues 677-690, see Figures 1 and 3~~Figures 3 and~~

~~5~~), albeit with low expectation value (0.63). Sequence alignment with entries from the Prosite database indicated that this motif represents only about a half of a typical myb domain.

Please amend the Specification at page 60, lines 17-20 in the following manner:

The Scc_ PCC 7942_Ftn2 also possesses a single TPR repeat (residues 136-169) as determined by the InterProScan program, and a leucine zipper pattern (residues 234-255) as determined by the Prosite-Protein against PROSITE program (http://ca.expasy.org/tools/scnpsite.html/).

Please amend the Specification at page 86, lines 14-27 in the following manner:

Immunoblotting with leaf tissue extracts and immunofluorescence microscopy of leaf mesophyll chloroplasts were performed as previously described (Stokes et al. (2000) Arabidopsis Plant Physiol. 124:1668-1677; Vitha et al.(2001) J. Cell. Biol.153:111-119) using rabbit antipeptide antibodies specific to AtFtsZ1 and AtFtsZ2 (antibodies were designated 1-1A and 2-1A, respectively). For immunofluorescence labeling, a goat anti-rabbit Oregon Green 488 conjugate (Molecular Probes, Eugene, OR) was used at 1:200 dilution. Specimens were viewed with Olympus BH-2 and Leica DMR A2 microscopes equipped with epifluorescence illumination, 100x oil immersion objectives, FITC fluorescence filter sets (excitation 455-495 nm, emission 512-575 nm) and CCD cameras Optronics (Goleta, CA) DEI 750 and Qimaging (Burnaby, B.C., Canada) Retiga 1350ex, respectively. The images were taken either as a single optical section or as a stack of images with spacing 0.5 μm between slices. Image stacks were processed and projected (Brightest Point method) with ImageJ ver. 1.27 software (http://rsb.info.nih.gov/ij/) and further adjusted and cropped using Adobe Photoshop 6.0 (Adobe Systems Inc., San Jose, CA).

Please amend the Specification at page 87, lines 2-13 in the following manner:

DNA and protein sequence databases were searched with tblastn and blastn (Altschul et al. (1990) J. Mol Biol. 215:403-10) at National Center for Biotechnology

Information (NCBI; at http://, followed by, www.ncbi.nlm.nih.gov), and in the *Arabidopsis thaliana* database at Munich Information Center for Protein Sequences (MIPS; at http://, followed by, mips.gsf.de/proj/thal/db/index.html). Preliminary sequence data for *Synechococcus* sp. strain WH8102, strain MED4, *Protochlorococcus marinus* strain MT9313 and *Nostoc punctiforme* strain ATCC 29133 were obtained from the DOE Joint Genome Institute (JGI) (at http://www, followed by, .jgi.doe.gov/JGI_microbial/html/index.html). The *Anabena* sp. PCC 7120 sequence was obtained from the Kazusa DNA Research Institute, Japan (at http://www, followed by, .kazusa.or.jp/cyano/). The preliminary *Synechococcus* sp. PCC 7002 sequence was obtained from NCBI through a tblastn search of microbial genomes (http://www, followed by, .ncbi.nlm.nih.gov/cgi-bin/Entrez/genom_table_cgi).

Please amend the Specification at page 87, line 14 through page 88, line 4 in the following manner:

For predictions of subcellular protein targeting, TargetP ver. 1.01 (Emanuelsson et al. (2000) J. Mol Biol. 300:1005-16) (at http://www, followed by, .cbs.dtu.dk/services/TargetP/) and Predotar ver. 0.5 (at http://www, followed by, .inra.fr/Internet/Produits/Predotar/) were used. Prediction of transmembrane domain was performed with HMMTOP ver. 2.0 (Tusnady and Simon (1998) J. Mol Biol. 283:489-506; Tusnady and Simon (2001) Bioinformatics 17:849-50) (at http://www, followed by, .enzim.hu/hmmtop/), TMHMM ver. 2.0 (Krogh et al. (2001) J. mol Biol. 305:567-580) (at http://www, followed by, .cbs.dtu.dk/services/TMHMM-2.0/), DAS (Cserzo et al. (1997) Pro t Eng. 10:673-676) (at http://www, followed by, .sbc.su.se/~miklos/DAS/), SOSUI (Hirokawa et al. (1998) Bioinformatics 14:378-379(at http://, followed by, sosui.proteome.bio.tuat.ac.jp/sosuiframe0E.html), Split (Juretic et al. (2002) J. Chem Inf Comp Sci: in press) (at http, followed by, ://pref.etfos.hr/split-4.0/); TMPRED (Hofmann and Stoffel (1993) Biol Chem Hoppe-Seyler 374:166) (at http://www, followed by, .ch.embnet.org/software/TMPRED_form.html) and TopPred2 (Claros and von Heijne (1994) Comput Appl Biosci 10:685-686) (at http://, followed by, bioweb.pasteur.fr/seqanal/interfaces/toppred.html). Identification of conserved domains

was facilitated by searches in the ProDom Protein domain database (Corpet et al. (2000) Nucleic Acids Res. 28:267-9) (at http:// , followed by, prodes.toulouse.inra.fr/prodom/doc/prodom.html) and through the Conserved Domain Database and Search Service, v1.54 at NCBI (at http://www, followed by, .ncbi.nlm.nih.gov/Structure/cdd/cdd.shtml). The PredictProtein service (at http://www, followed by, .embl-heidelberg.de/predictprotein/predictprotein.html) was further used as interface to access multiple tools for the primary and secondary structure analysis.

Please amend the Specification at page 88, lines 5-17 in the following manner:

The exon/intron prediction for the rice *Ftn2* homologue from the genomic DNA sequence combined results from several algorithms: GeneScan (Burge and Karlin (1997) J Mol Biol. 215:403-10) (at http:// , followed by, genes.mit.edu/GENSCAN.html), GrailEXP v3.3 (Xu and Uberbacher (1997) J Compt Biol. 4:325-38) (at http:// , followed by, compbio.ornl.gov/grailexp/), FGENESH 1.1 (at http:// , followed by, genomic.sanger.ac.uk/gf/gf.shtml) and Genie (Kulp et al. (1996) Proc Int Conf Intell Syst Mol Biol. 4:134-42) (at http:// , followed by, www.fruitfly.org/seq_tools/genie.html). The exon/intron predictions were then compared to the available rice ESTs and to the homology regions with the *Arabidospis* AtFtn2 identified in tblastn search. Sequence manipulation, multiple alignments and shading of aligned sequences were performed using BioEdit 5.09 (at http:// , followed by, www.mbio.ncsu.edu/BioEdit/bioedit.html). DNA sequencing reads were processed using the Phred basecaller (Ewing et al. (1998) Genome Res. 8:175-185, assembled with Phrap assembler and contig assemblies then viewed with Consed (at http://www, followed by, .phrap.org/).

Please amend the Specification at page 90, lines 5-11 in the following manner:

The *AtFtn2* genomic sequence has 6 exons (Figure 1~~Figure 3~~). The presence of EST and full length cDNA in the sequence database (Table 3 below) indicates that the gene is expressed. Both the predicted and the experimentally determined full length cDNA coding sequences (Table 3 below) have 2406 nt encoding a protein of 801 aa, with putative N-terminal chloroplast targeting sequence of 67 aa predicted by TargetP.

Chloroplast targeting was also predicted by Predotar (targeting scores 0.738 and 0.979 for TargetP and Predotar, respectively).

Please amend the Specification at page 90, lines 12-20 in the following manner:

A search for protein motifs with InterProScan revealed a putative DnaJ domain (AtFtn2 residues 89-153), InterPro accession IPR001623, Pfam conserved domain pfam00226. However, ClustalW alignment of this domain with all predicted DnaJ domains from the Pfam database (277 sequences) revealed that the central Histidine-Proline-Aspartate (HPD) motif typical for DnaJ proteins is not present in *AtFtn2* or in other plant and cyanobacterial *Ftn2* homologues (Figure 2~~Figure 4~~). In addition to the DnaJ-like domain, the Pfam-HMM search identified a putative myb domain (residues 677-690, see Figure 2~~see Figure 4~~) albeit with low expectation value (0.63). Sequence alignment with myb domains from the Prosite database indicated that only a second half of the putative myb domain is present in AtFtn2.

Please amend the Specification at page 94, lines 2-16 in the following manner:

[1] Standard Arabidopsis ORF name (http:// , followed by, arabidopsis.org/info/guidelines.html)
[2] Type of DNA sequence: EST (Expressed Sequence Tag), cDNA (full length cDNA), Gen (Genomic DNA)
[3] Unfinished fragment of the genome, Joint Genome Institute (JGI)
[4] Draft analysis; http:// , followed by, genome.ornl.gov/microbial/npun/31may01/npun.html
[5] draft analysis http:// , followed by, genome.ornl.gov/microbial/pmar_med/
[6] Draft analysis http:// , followed by, genome.ornl.gov/microbial/pmar_mit/
[7] AAAA0100502 Predicted Gen sequence from shotgun sequencing data, see Methods; BK000999 cDNA sequence
[8] complement (211130..213526)
[9] complement (3300430..3302826)
[10] complement (2314780..2316924)
[11] complement (47521..49665)
[12] bases 6632806..6639031
[13] bases 64077..67114; gene id: MDH9.18

Please amend the Specification at page 95, lines 8-12 in the following manner:

ClustalW alignment of full and partial Ftn2 protein sequences (Figure 3~~Figure 5~~) showed that the N- terminal, and to a lesser degree also the C-terminal, regions of these proteins are conserved and separated by a highly divergent central area (Figure 1B~~Figure 3B~~). The cyanobacterial homologues shared approximately 20% identity and 40 % similarity with AtFtn2, while scores for the rice homologue were 47% and 68%, respectively (Table 4).

Please amend the Specification at page 102, line 28 through page 103, line 4 in the following manner:

In FTN2 and FTN6, the transposon was inserted in single-copy open reading frames (ORFs) that were denoted *Ftn2* and *Ftn6*. *Ftn2* predicts a 631-amino acid protein (SEQ ID NO: 5~~see Figure 6, panel B~~) that shows greatest similarity to the predicted products of an ORF designated $Ftn2_A$ from *Anabaena* sp. strain PCC 7120 (bp 3302826-3300430 in the chromosome ~~(see Figure 8)~~; BLAST score, 278; Expect = 3×10^{-75}; [1]), a *Nostoc punctiforme* ORF (BLAST score, 263; Expect = 1×10^{-70}), and presumptive gene *sll0169* of *Synechocystis* sp. strain PCC 6803 (BLAST score, 218; Expect = 2×10^{-55}).

Please amend the Specification at page 103, lines 5-12 in the following manner:

The InterProScan program (http://www, followed by, .ebi.ac.uk/interpro/scan.html) shows the presence in Ftn2 of a DnaJ N-terminal domain (amino acid residues 6-70) and a single TPR repeat (amino acid residues 136-169. The Prosite-Protein against PROSITE program (http://ca.expasy.org/tools/scnpsite.html/) shows the presence in Ftn2 of a leucine zipper pattern (amino acid residues 234-255; Table 7). Ftn2 and its cyanobacterial and plant orthologs show the presence of a DnaJ N-terminal domain, but are otherwise, as are Ftn6 and its orthogs, dissimilar from the products of known division-related genes (Bramhill D (1997) Annu. Rev. Cell. Dev. Biol. 13:395-424).

Please amend the Specification at page 108, lines 4-14 in the following manner:

To determine whether the wild type *ARC5* gene could complement the mutation, the predicted *ARC5* gene (a transgene containing the predicted At3g19730 /At3g19720

locus plus 1.9 kb and 1.1 kb of the 5' and 3' flanking DNA, respectively) was amplified from the DNA of BAC MMB12 by PCR using the primers 5'-GGAATTCCGAGTCGAGTTGCTTTGTTG-3' and 5'-CGTCTAGAGCTTACCTCAAAGGTACATGGA-3'. The PCR product was digested with *Eco*RI and ligated into a derivative of the transformation vector pLH7000 (http://www, followed by, .dainet.de/baz/jb2000/jb_2000direkt.htm) digested with *Eco*RI and *Sma*I. The construct was transferred to *A. tumefaciens* GV3101 and introduced into *arc5* plants by floral dipping. The phenotypes of the T_1 plants were determined by microscopy. Microscopic analysis of T_1 transgenic plants indicated that the chloroplast division defect in the mutant was fully or partially rescued by the wild-type transgene.

Please amend the Specification at page 108, line 29 through page 109, line 19 in the following manner:

The protein sequences were blasted against the NCBI protein database. The amino acid sequences of ARC5 were deduced from the cDNA sequence; the long form of the cDNA encodes a protein of 777 amino acids and 87.2 kDa, whereas the shorter form of the cDNA encodes a protein of 741 amino acids and 83.5 kDa. The sequence alignment was performed with the CLUSTALW multiple alignment program (Thompson, J. D. *et al.* (1994) *Nucleic Acids Res.* 22, 4673-4680) at the Biology Workbench 3.2 website (http:// , followed by, biowb.sdsc.edu/). Protein sequences used for the phylogenetic analysis were aligned with Clustal X (Thompson, J. D. *et al.* (1997) *Nucleic Acids Res.* 25, 4876-4882) using default settings. Neighbor joining and maximum parsimony analyses were performed using PAUP version 4.0b10 (Swofford, D. L. (1998) *PAUP*. Phylogenetic Analysis Using Parsimony (*and Other Methods). Version 4.0b10* (Sinauer Associates, Sunderland, Massachusetts)) with default settings except for ties being randomly broken. Neighbor-joining and maximum parsimony analyses produced topologically identical trees. Bootstrap analyses were performed on the neighbor-joining and maximum parsimony trees with one thousand replications. GENBANK® accession numbers for proteins aligned with ARC5 (longer form, accession no. AY212885) are as follows: human Dynamin-1 (NP_004399), yeast Dnm1p (NP_013100), At1g53140

(NP_175722), rice dynamin like protein (BAB56031), ADL6 (AAF22291), At5g42080 (NP_568602), *Glycine* phragmoplastin (AAB05992), tobacco phragmoplastin (CAB56619), At2g44590 (NP_181987), human Dynamin II (NP_004936), ADL2a (NP_567931), ADL2b (NP_565362), rice ADL2-like protein (BAB86118), worm Drp-1 (AAL56621) and human Dnm1p/Vps1p-like protein (JC5695).

Please amend the Specification at page 110, line 17 through page 111, line 13 in the following manner:

The subcellular localization of ARC5 was investigated by expressing a GFP-ARC5 fusion protein in transgenic plants. The GFP sequence was amplified from plasmid smRS-GFP (Davis, S. J. & Vierstra, R. D. (1998) *Plant Mol. Biol.* 36, 521-528) with the primers 5'-CGGGATCCATGAGTAAAGGAGAAGAACT-3' and 5'-GCTCTAGATAGTTCATCCATGCCATGT-3'. The PCR product was digested with *Bam*HI and *Xba*I. The *ARC5* coding region and 1.1 kb of the 3' flanking DNA were amplified from the MMB12 BAC clone with primers 5'-GGACTAGTACGATGGCGGAAGTATCAGC-3' and 5'-CGGGATCCGCACCGAAGGAGCCTTTAGATT-3'. The PCR product was digested with *Spe*I and *Eco*RI. cDNA fragments encoding GFP and ARC5 were subcloned into Bluescript KS+ (Stratagene) that had been digested with *Eco*RI and *Bam*HI to create a *GFP-ARC5* fusion construct. The *ARC5* promoter was amplified from MMB12 with primers 5'-GACTAGTTGGCTCAACGCTTACCTCAA-3' and 5'-CGGGATCCGCCATCGTCTCTTACGA-3', and cloned into Bluescript KS+ (Stratagene) between the *Spe*I and *Bam*HI sites. The promoter fragment was then subcloned into the plasmid containing the *GFP-ARC5* fusion construct at the 5' end of the fusion. The resulting plasmid was digested with *Spe*I and *Eco*RI, and the promoter-*GFP-ARC5* cassette was subcloned into a derivative of the transformation vector pLH7000 (http://www, followed by, .dainet.de/baz/jb2000/jb_2000direkt.htm). The plasmid was transferred to *A. tumefaciens* GV3101 and used to transform wild-type *A. thaliana* plants (Col-0) as described above. The GFP-ARC5 localization pattern was visualized by fluorescence microscopy in T_1 plants. For *in vivo* detection of green

fluorescent protein (GFP), fresh leaf tissue was mounted in water and viewed with an L5 filter set (excitation 455 nm to 495 nm, emission 512 to 575 nm) and a 100X oil immersion objective of a Leica DMR A2 microscope (Leica Microsystems, Wetzlar, Germany) equipped with epifluorescence illumination. Images were captured with a cooled CCD camera (Retiga 1350EX, Qimaging, Burnaby, British Columbia, Canada) and processed with Adobe Photoshop imaging software (Adobe Systems, San Jose, CA).

Please amend the Specification at page 113, line 3 in the following manner:

Table 10 **ARC5**		
Gene	**SEQ ID NO**	~~**Figure Number**~~
ARC5 Genomic (BAC MMB12(GB:AP000417))	11	~~9~~
ARC5 cDNA	12	~~10~~
ARC5 Protein	13	~~11~~
NCBI ARC5 Genomic (BAC MMB12(GB:AP000417))	14	~~12~~
NCBI ARC5 cDNA	15	~~13~~
NCBI ARC5 Protein	16	~~14~~
NCBI ARC5 Homologue (protein)	17	~~15~~
MIPS ARC5 Homologue (protein)	18	~~16~~
ARC5 Genomic [1]	26; 27 [2]	~~24~~

Please amend the Specification at page 115, line 7 in the following manner:

Table 11 **Fzo-Like Gene**		
Gene	**SEQ ID NO**	~~**Figure Number**~~

MIPS Fzo Genomic	19	~~17~~
MIPS Fzo cDNA	20	~~18~~
MIPS Fzo Protein	21	~~19~~
NCBI Fzo Genomic	22	~~20~~
NCBI Fzo cDNA	23	~~21~~
NCBI Fzo Protein	24	~~22~~
3' Fzo Genomic (BAC F15K9)	25	23